

Applicants request entry of this amendment in adherence with 37 C.F.R. §§1.821 to 1.825. This amendment is accompanied by a floppy disk containing the above named sequences, SEQ ID NOS:1-10, in computer readable form, and a paper copy of the sequence information which has been printed from the floppy disk.

The information contained in the computer readable disk was prepared through the use of the software program "PatentIn" and is identical to that of the paper copy. This amendment contains no new matter.

Attached hereto is a marked-up version of the changes made to the Specification and Abstract by the current Amendment. The attached pages are captioned **"VERSION WITH MARKINGS TO SHOW CHANGES MADE."**

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,



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**VERSION WITH MARKINGS TO SHOW CHANGES MADE**

**In the Specification:**

Paragraph (Table 1) beginning at line 2 of page 8 has been amended as follows (see attached sheet, Table 1):

Paragraph (Table 2) beginning at line 2 of page 10 has been amended as follows (see attached sheets, Table 2):

Paragraph (Table 3) beginning at line 2 of page 13 has been amended as follows (see attached sheet, Table 3):

Paragraph (Table 4) beginning at line 1 of page 14 has been amended as follows (see attached sheet, Table 4):

Table 1: Nucleotide sequence (SEQ ID NO:1) encoding a murine CTLA-8 protein and predicted amino acid sequence (SEQ ID NO:2). Also can use complementary nucleic acid sequences for many purposes. Submitted to GenBank/EMBL under accession number L13839.

1 GAATTCATC CATGTGCTG ATGCTGTTGC TCTACTGAA CTTGAGGCT ACAGTGAAGG  
61 CAGCGGTACT CATCCCTCAA AGTTCAGTGT GTCCAAACGC CGAGGCCAAT AACTTTCTCC  
121 AGAAGCTGAA GGTCAACCTG AAAGTCATCA ACTCCCTTAG CTCAAAAGCG AGCTCCAGAA  
181 GGTCCCTCAGA CTACCTCAAC CGTTCACCTT CACCCCTGGAC TCTGAGGCGC AATGAGGACC  
241 CTGATAGATA TCCTTCTGTG ATCTGGGAGG CACAGTGGCG CCACCAACGC TGTGTCAACG  
301 CTGAGGGGAA GTTGGAGCAC CACATGAATT CTGTTCTCAT CCAGCAAGAG ATCCTGCTCC  
361 TGAAGAGGGA GCTTGAAGA TGCCCTTCA GTTCCGGGT GGAAGAATG CTGGTGGGG  
421 TGGGCTGCAC CTGCTTTTC TCTATTGTG GCCATGGCTC CTAAACAGAG ACCTGAGGCT  
481 AGCCCTAAG AAACCCCTGC GTTCTCTGC AAACCTCCTT GTCTTTTAA AACAGTTCAC  
541 AGTTGAATCT CAGCAAGTGA TATGGATTTA AAGGGGGGT TAAATTTGTC TGCTTCCAC  
601 CCTGAAAAGA AGGCGCAGAG GGGATATAAA TTGCTTCTG TTTTCTGTG GGCTTTAAAT  
661 TATTTATGTA TTTACTCTAT CCGAGATAA GTTGAAGCA TAAATTATTT TAATGAATTA  
721 TCTACATTAT TATTATGTTT CTTAATGAG AAGACAAAAT TCAAGACTAA GAAATTTTAT  
781 TATTTAAAAG GTAAACCTA TATTTATATG AGCTATTTAT GGGTCTATTT ATTTTCTTC  
841 AGTGCTAAGA TCATGATTAT CAGATCTACC TAAGGAAGTC CTAAATAATA TTAAATATTA  
901 ATTGAAATTT CAGTTTACT ATTTGCTTAT TAAAGTTCC CTCCTCTGAA TGGTGTGAAA  
961 TCAAACCTCG TTTTATGTTT TTAAATTATT GAGGCTTCGA AAAATTGGGC AATTTAGCTT  
1021 CCTACTGTGT GTTTAAAAAC CTTGTAACAA TATCACTATA ATAAATTTTT GGAAGAAAAT

Predicted amino acid sequence (150 amino acids) (SEQ ID NO:2). Mature polypeptide probably starts at about amino acid 13 (Ala).

MCLML LLLLN LEATV KAAVL IPQSS VCPNA EANNF LQNVK VNLKV INSL  
SKASS RRPST YLNRS TSPWT LSRNE DPDRY PSVIW EAQCR HQRCV NAEGK  
LDHMH NSVLI QQEIL VLKRE PEKCP FTFRV EKMLV GVGCT CVSSI VRHAS

Table 2: Nucleotide sequence (SEQ ID NO:3) of the related herpesvirus Saimiri open reading frame ORF13 and predicted amino acid sequence (SEQ ID NO:4) of encoded protein, see GenBank/EMBL accession number M60286.

herpesvirus

AGCTTCATGC AAATACATCT TATCTTACCA GATTCTCGCC TCATTGCAA 50  
ACATGCCTCA TCTTTTGAGA AGAAACGCAA TTCGAACTTC TTCTAATGCT 100  
CCTGAAGAGC AGCCTGTGCT GCAGCCTGAG CTTGATGCTA TTGAAGAGCT 150  
AGAATAAGAG CTATTTTTTG ACGATGGGTG CTGCCTTTCT GTTCAAGAAA 200  
TCTGCTTAAT TCTTCTTGA TTCTTATTGT TTCTGCTAGC TGTAATTGTT 250  
TTTTATAACT ATACAGACAC AGATCAATTT GTGAAGCTGA CACATCTTAT 300  
GAGCCACAAA AATTCTATCA AAGGACCTTT TGATCTTTAA GGTATGTAAT 350  
CATAATTTTA TTTTTTTATT TCTAAACAA TCTTAGTATA TATAATTAAT 400  
ACAAATTTTA GAAAATACTA TAATAAATAT TGAAAGCTGT ATTTACATTG 450  
TAAACTATAT ATAGGCAATG TAAAGTCATT CTAACCTTAG GTTTGCTTTA 500  
CCTGTTACAG AAACCTCACC TGTGTGTCAA GAGCTGCAA CATGGCTTTA 550  
GACTTAAGAA ATCTTAAACA CCTGACTGCT AACTTCAGTT TTAGAATAAT 600  
GATATGGATT ATGCTATGTT TGGCTCTACC TACTGATAGT AAACCTATTT 650  
CAACAACCTGA AGCTCCAATA CTAAACATAA CACAATCTCC AAGTTTGAAC 700  
ATCTCATCAC CTTCTACTTT AGAACCTTCA GAGCTCTTA AAAACTGTAC 750  
AACATTCTTA GACTTACTTT GGCAGCGGCT GGGCGAGAAC GCTTCTATAA 800  
AGGACTTGAT GTTAACATTA CAACGAGAAG AAGTCCACGG AAGAATGACT 850  
ACACTTCCTT CACCTAGACC AAGCAGTAAA GTTGAAGAAC AACAGTTACA 900  
AAGACCTAGA AACTTACTGC CTACTGCTGT CGGGCCACCT CATGTCAAAT 950  
ATAGACTATA TAATCGCTTA TGGGAAGCTC CTAAAGGAGC TGATGTTAAT 1000  
GGTAAACCTA TACAATTGTA TGACCCTCCT CTTCTTATA CAGGGGCATA 1050  
TAATGATGAT GGTGTTTTAA TGGTTAATAT TAATGGAAAA CATGTGAGGT 1100  
TTGATAGCTT GTCTTATTGG GAAAGAATTA AAAGATCTGG TACCCCATGG 1150  
TGTATAAAGA CACCAAGTGA AAAAGCAGCA ATATTGAAGC AGCTTTTAAA 1200  
AGCTGAAAAA AAATGTAGGA CTACTTCTAA ACGTATCACT GAGTTAGAAG 1250

Table 2, continued:

AGCAGATTAA AGAACTAGAA AAAACTAGTA CATCTCCATA GATTATGTGTT 1300  
AGAATGTGTT TATCATACTA AAATAAATGC TTTATGTATT GCAATATTAC 1350  
TTGTTTGCTA TGACTTTGGT ATATGAAATG CAAATCTTAA ATAAAAAGTT 1400  
TTTGTCTAGT ATTG3CGTCA CTGTATTTTA CTAGCAAAAA TATATAAATT 1450  
GTTATGTAGC AAGAAGTTTG TATCAATATA AAAACTCTAA AGTATATAAA 1500  
CAAACATTCA ATTAGTGTA ATCATAGCAA GCATATCTTT TCATACGTGT 1550  
CTAGTTAATT TAAAGAATTA ATTATGACAT TTAGAATGAC TTCACCTTGT 1600  
TTACTTCTGC TGCTGAGCAT AGATTGTATA GTAAAGTCAG AAATAACAA 1650  
CGCACAAACC CCAAGATGCT TAGCTGCTAA CAATAGCTTT CCACGCTCT 1700  
TGATGGTTAC TTTGAGCATC CGTAACTGGA ATACTAGTTC TAAAA3GGT 1750  
TCAGACTACT ACAATAGATC TACGTCTCCT TGGACTCTCC ATCGCAATGA 1800  
AGATCAAGAT AGATATCCCT CTGTGATTG GGAAGCAAAG TGTCGCTACT 1850  
TAGGATGTGT TAATGCTGAT GGGAATGTAG ACTACCAT GAACTCAGTC 1900  
CCTATCCAAC AAGAGATTCT AGTGGTGCGC AAAGGGCATC AACCTGCTC 1950  
TAATTCATTT AGGCTAGAGA AGATGCTAGT GACTGTAGGC TGCACATGCG 2000  
TTACTCCCAT TGTTCACAAT GTAGACTAAA AGCTATCTAA ATTTTGAAAA 2050  
TTAACATTTC ACTAAAAAC AAAAAGTTGA TTTTTTCTT TTAAATAAAA 2100  
AAAGTTTAAAT ATAAGTTCTG GCTTGTTTGG TTTTGGACTA ATCAATGTAG 2150  
ATCACACTTG T3ATCTTAGC TCTCGGAAG CAATGTAAGA AAATATATTT 2200  
AACTTAAGAG TTTTAGACTT GCTTGASTTT TATGASTAAA AAACAAAGAA 2250  
TAAGCACAGC TTCTTGATC TTCTTTTAAA AACTTTAAGT TATTTATGTA 2300  
TTTAATATAA TCTAATGTTT CTTAAACATG TTGAGTTTGA GGTCCACTAA 2350  
TACAACATTA TAATTTTTTC TGTTATAACA CTTTTGCAAG AAGAACTCAT 2400  
TTTATAGAAA ATGAGCAGTA TTCAAAAAAA ATGTTTGATA TGCTGTAATA 2450  
TTGGAGAGGA AGAACTTTTA CAAGCATGTG ATTGTCCTAG CAGAGTCCAT 2500  
CATACATGCT TACAAAGTCA 2520

Table 2, continued:

Predicted predicted amino acid sequence (SEQ ID NO:4) of encoded protein of  
the related herpesvirus Saimiri open reading frame ORF13

MTFRM TSLVL LLLLS IDCIV KSEIT SAQTP RCLAA NNSFP RSVMV TLSIR 50

NWNTS SKRAS DYYNR STSPW TLHRN EDQDR YPSVI WEAKC RYLGC VNADG 100

NVDYH MNSVP IQQEI LVVRK GHQPC PNSFR LEKML VTVGC TCVTP IVHNV 150

D

151

Table 3: Nucleotide sequence (SEQ ID NO:5) of human CTLA-8 fragment and predicted amino acid sequence (SEQ ID NO:6) of encoded protein.

AGC/CGC AAT GAG GAC CCT GAG AGA TAT CCC TCT GTG ATC TGG GAG  
GCA AAG TGC CGC CAC TTG GGC TGC ATC AAC GCT GAT GGG AAC GTG  
GAC TAC CAC ATG AAC TCT GTC CCC ATC CAG CAA GAG ATC CTG GTC  
CTG CGC AGG GAG CCT CCA CAC TGC CCC AAC TCC TTC CGG CTG GAG  
AAG ATA CTG GTG TCC GTG GGC TGC ACC TGT GTC ACC CGG ATT GTC  
CAC CAT GTG GCC TAA

ser/arg asn glu asp pro glu arg tyr pro ser val ile trp glu  
ala lys cys arg his leu gly cys ile asn ala asp gly asn val  
asp tyr his met asn ser val pro ile gln gln glu ile leu val  
leu arg arg glu pro pro his cys pro asn ser phe arg leu glu  
lys ile leu val ser val gly cys thr cys val thr pro ile val  
his his val ala OCH

This was used to isolate a full length clone from human (SEQ ID NO:7),  
shown below with its predicted amino acid sequence (SEQ ID NO:8); SEQ ID  
NO:5 corresponds to nucleotides 272-510 of SEQ ID NO:7:

GG CACAAACTCA TCATCCCA GTTGATTGGA AGAAACAACG 42

ATG ACT CCT GGG AAG ACC TCA TTG GTG TCA CTG CTA CTG CTG CTG 87  
Met thr pro gly lys thr ser leu val ser leu leu leu leu leu 15

AGC CTG GAG GCC ATA GTG AAG GCA GGA ATC ACA ATC CCA CGA AAT 132  
ser leu glu ala ile val lys ala gly ile thr ile pro arg asn 30

CCA GGA TGC CCA AAT TCT GAG GAC AAG AAC TTC CCC CGG ACT GTG 177  
pro gly cys pro asn ser glu asp lys asn phe pro arg thr val 45

ATG GTC AAC CTG AAC ATC CAT AAC CGG AAT ACC AAT ACC AAT CCC 222  
met val asn leu asn ile his asn arg asn thr asn thr asn pro 60

aa AGG TCC TCA GAT TAC TAC AAC CGA TCC ACC TCA CCT TGG AAT 267  
lys arg ser ser asp tyr tyr asn arg ser thr ser pro trp asn 75

CTC CAC CGC AAT GAG GAC CCT GAG AGA TAT CCC TCT GTG ATC TGG 312  
leu his arg asn glu asp pro glu arg tyr pro ser val ile trp 90

GAG GCA AAG TGC CGC CAC TTG GGC TGC ATC AAC GCT GAT GGG AAC 357  
glu ala lys cys arg his leu gly cys ile asn ala asp gly asn 105

GTG GAC TAC CAC ATG AAC TCT GTC CCC ATC CAG CAA GAG ATC CTG 402  
val asp tyr his met asn ser val pro ile gln gln glu ile leu 120

GTC CTG CGC AGG GAG CCT CCA CAC TGC CCC AAC TCC TTC CGG CTG 447  
val leu arg arg glu pro pro his cys pro asn ser phe arg leu 135

GAG AAG ATA CTG GTG TCC GTG GGC TGC ACC TGT GTC ACC CGG ATT 492  
glu lys ile leu val ser val gly cys thr cys val thr pro ile 150

GTC CAC CAT GTG GCC TAA 510  
val his his val ala OCH 155

Table 4: Nucleotide sequence (SEQ ID NO:9) of mouse CTLA-8 fragment and predicted amino acid sequence (SEQ ID NO:10) of encoded protein.

gaggctcaagtgcacccagcaccagctgatcaggacgcgcaaacatgagtcacagggagagcttcatctg 69  
 tgtctctgatgctgttctgctgctgagcctggcgggtacagtggaaggcagcagcgatcatccctcaaa 138  
 gctcagcgtgtccaaacactgaggccaaggacttctccagaatgtgaagggtcaacctcaaagtcttta 207  
 actccctTGGCGCAAAAGTGAGCTCCAGAAgGCCCTCAGACTACCTCAACCGTTCCACGTCACCTGGA 276  
 CTCTCCACCGCAATGAAGAcCCTGATAGATATCCCTCTGTGATCTGGGAAGCTCAGTGCCTGCCACCAGE 345  
 GCTGTGTCAATGCGGAGGgaaagctggaccaccacatgaattctgtttctcatccagcaagagatcctgg 414  
 tctgaagaggagcctgagagctgccccttcaactttcaggggtcgagaagatgctgggtgggTGTGGGCT 483  
 GCACCTGCGTG3CCTCGATTGTCCG3CAGG3CAGCCTAAACAGAGACCCG3G3CTGACCCCTAAGAAACC 552  
 CCCACGTTTCTCAGCAAACCTTACTTCCATTTTTTAAAACAGTTCGTGTATTGATTTTCAGCAAGGAATG 621  
 TGGATTGAGAG3CAGATTGAGAATTGTCTGCCCTCCACAATGAAAA3AAG3TGTAAAG3G3TCCCAAACT 690  
 TGCTTCgtgtttgtttttctgtggactttaattattttgtgtattttacaatatccaagataactttga 759  
 aggcgtaacttatttaatagaagtatctacattattattatgtttctttctgaagaagacaaaattcaag 828  
 actcagaaattttattattttaaaaggttaagcctatatttatatgaggtattttatgaattctattttttt 897  
 tcttcagttattgaagtatttaagaacatgattttCAGATCTACCTAGGGAA3TCTTA3TAAGATTAAA 966  
 TATTAATGGAAATTTTACGCTTTACTATTGTGTTGATTAAAGGTTCTCTCTCTGAAATGG3GTGAAACC 1035  
 AAACCTAGTTTTATGTTTAATAACTTTTTAAATTATTGAAGATTCAAAAAATTGGATAATTTAGCTCCC 1104  
 TACTCTGTTTTAAAAAAAAAAAAAAAAAAAAA 1134

Mouse CTLA-8 predicted amino acid sequence (SEQ ID NO:10). The mature polypeptide probably starts at a position about amino acid 19 (Leu) to amino acid 21 (Ala).

METSerProGlyArgAlaSerSerValSerLeuMETLeuLeuLeuLeuLeuSerLeuAlaAlaThrValLys 24  
 AlaAlaAlaIleIleProGlnSerSerAlaCysProAsnThrGluAlaLysAspPheLeuGlnAsnValLys 48  
 ValAsnLeuLysValPheAsnSerLeuGlyAlaLysValSerSerArgArgProSerAspTyrLeuAsnArg 72  
 SerThrSerProTrpThrLeuHisArgAsnGluAspProAspArgTyrProSerValIleTrpGluAlaGln 96  
 CysArgHisGlnArgCysValAsnAlaGluGlyLysLeuAspHisHisMETAsnSerValLeuIleGlnGln 120  
 GluIleLeuValLeuLysArgGluProGluSerCysProPheThrPheArgValGluLysMETLeuValGly 144  
 ValGlyCysThrCysValAlaSerIleValArgGlnAlaAla 158



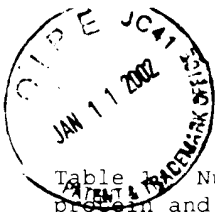


Table 1. Nucleotide sequence (SEQ ID NO:1) encoding a murine CTLA-8 protein and predicted amino acid sequence (SEQ ID NO:2). Also can use complementary nucleic acid sequences for many purposes. Submitted to GenBank/EMBL under accession number L13339.

1 GAATTCCATC CATGTGCCTG ATGCT3TTGC TGCTACTGAA CCTG3AGGCT ACAGT3AAGG  
61 CAGCGGTACT CATCCCTCAA AGTTCAGTGT GTCCAAAAGC CGAG3CCAAT AACTTTCTCC  
121 AGAACGTGAA GGTCAACCTG AAAGTCATCA ACTCCCTTAG CTCAAAAGCG AGCTCCAGAA  
181 GGCCCTCAGA CTACCTCAAC CGTTCCACTT CACCCTGGAC TGT3AGCCGC AAT3AGGACC  
241 CTGATAGATA TCCTTCTGTG ATCTG33AG3 CACAGT3CC3 CCACCAGCGC TGTGTCAACG  
301 CTGAGGGGAA GTTGGACCAC CACAT3AATT CTGTTTCTCAT C3A3CAAGAG ATG3T3GTCC  
361 TGAAGAGGGA GCCTGAGAAG TGCCCTTTCA CTTTCC3G3T G3A3AAGAT3 CTG3T3G3CG  
421 TGGGCTGCAC CTGCGTTTCC TCTATT3TCC G3CAT3G3TC CTAACAGAG ACCTG33CT  
481 AGCCCCTAAG AAACCCCTGC GTTTCTCTGC AAACCTTCTT GTTTTTTAA AACAGTTCAC  
541 AGTTGAATCT CAGCAAGTGA TATGGATTTA AAGGCG3GGT TACAATTGTC TGCCTTCCAC  
601 CCTGAAAAGA AGGCGCAGAG GGGATATAAA TTGCTTCTTG TTTTCTGTG GGCTTTAAAT  
661 TATTTATGTA TTTACTCTAT CCCGAGATAA CTTTGAGGCA TAAGTTATTT TAATGAATTA  
721 TCTACATTAT TATTATGTTT CTTAATGCAG AAGACAAAAT TCAAGACTAA GAAATTTTAT  
781 TATTTAAAAG GTAAAACCTA TATTTATATG AGCTATTTAT GGTCTATTT ATTTTCTTC  
841 AGTGCTAAGA TCATGATTAT CAGATCTACC TAAGGAAGTC CTAAATAATA TTAAATATTA  
901 ATTGAAATTT CAGTTTACT ATTTGCTTAT TTAAG3TTCC CTCCTCTGAA TGGTGT3AAA  
961 TCAAACCTCG TTTTATGTTT TTAAATTATT GAGGCTTCCA AAAATTGGGC AATTTAGTTT  
1021 CCTACTGTGT GTTTAAAAAC CTTGTAACAA TATCACTATA ATAAATTTTT G3AAGAAAAT

Predicted ~~predicted~~ amino acid sequence (150 amino acids) (SEQ ID NO:2).  
Mature polypeptide probably starts at about amino acid 13 (Ala).

MCLML LLLLN LEATV KAAVL IPQSS VCPNA EANNF LQNVK VNLKV INSL  
SKASS RRPST YLNRS TSPWT LSPNE DPDRY PSVIW EAQCR HQRCV NAEGK  
LDHHM NSVLI QQEIL VLKRE PEKCP FTFRV EKMLV GVGCT CVSSI VRHAS

Table 2: Nucleotide sequence (SEQ ID NO:3) of the related herpesvirus Saimiri open reading frame ORF13 and predicted amino acid sequence (SEQ ID NO:4) of encoded protein, see GenBank/EMBL accession number M60286.

herpesvirus

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AGCTTCATGC AAATACATCT TATCTTACCA GATTCTCGCC TCATTTGCAA 50
ACATGCCTCA TCTTTTGAGA AGAAACGCAA TTCGAACTTC TTCTAATGCT 100
CCTGAAGAGC AGCCTGTGCT GCAGCCTGAG CTTGATGCTA TTGAAGAGCT 150
AGAATAAGAG CTATTTTTTG ACGATGGGTG CTGCCTTTCT GTTCAAGAAA 200
TCTGCTTAAT TGTTCTTGGA TTCTTATTGT TTCTGCTAGC TGTAATTGTT 250
TTTTATAACT ATACAGACAT AGATCAATTT GTGAAGCTGA CACATCTTAT 300
GAGCCACAAA AATTCTATCA AAGGACCTTT TGATCTTTAA GGTATCTACT 350
CATAATTTTA TTTTTTTTAT TCTAAACAA TCTTAGTATA TATAATTAAT 400
ACAAATTTTA GAAAATACTA TAATAAATAT TGAAAGCTGT ATTTACATTG 450
TAAACTATAT ATAGGCAATG TAAAGTCATT CTAACCTTAG GTTGGCTTTA 500
CCTGTTACAG AAACCTCACC TGTGTGTCAA GAGCTGCAAA CATGGCTTTA 550
GACTTAAGAA ATCTTAAACA CCTGACTGCT AACTTCAGTT TTAGAATAAT 600
GATATGGATT ATGCTATGTT TGGCTCTACC TACTGATAGT AAACCTATTT 650
CAACAACTGA AGCTCCAATA CTAAACATAA CACAATCTCC AAGTTTGAAC 700
ATCTCATCAC CTTCTACTTT AGAACCTTCA GAGCCTCTTA AAAACTGTAC 750
AACATTCTTA GACTTACTTT GGCAGCGGCT GGGCGAGAAC GCTTCTATAA 800
AGGACTTGAT GTTAACATTA CAACGAGAAG AAGTCCACGG AAGAATGACT 850
ACACTTCCTT CACCTAGACC AAGCAGTAAA GTTGAAGAAC AACAGTTACA 900
AAGACCTAGA AACTTACTGC CTACTGCTGT CGGGCCACCT CATGTCAAAT 950
ATAGACTATA TAATCGCTTA TGGGAAGCTC CTAAAGGAGC TGATGTTAAT 1000
GGTAAACCTA TACAATTTGA TGACCCTCCT CTTCTTATA CAGGGGCATA 1050
TAATGATGAT GGTGTTTTAA TGGTTAATAT TAATGGAAAA CATGTGAGGT 1100
TTGATAGCTT GTCTTATTGG GAAAGAATTA AAAGATCTGG TACCCCATGG 1150
TGTATAAAGA CACCAAGTGA AAAAGCAGCA ATATTGAAGC AGCTTTTAAA 1200
AGCTGAAAAA AAATGTAGGA CTACTTCTAA ACGTATCACT GAGTTAGAAG 1250

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Table 2, continued:

AGCAGATTAA AGAACTAGAA AAAACTAGTA CATCTTCATA GATTACTGTT	1300
AGAATGTGTT TATCATACTA AAATAAATGC TTTATGTATT GCAATATTAC	1350
TTGTTTGCTA TGACTTTGGT ATATGAAATG CAAATCTTAA ATAAAAAGTT	1400
TTTGTCTAGT AITGGCGTCA CTGTATTTTA CTAGCAAAAA TATATAAATT	1450
GTTATGTAGC AAGAAGTTTG TATCAATATA AAAACTCTAA AGTATATAAA	1500
CAAACATTCA ATTAGTGTA ATCATAGCAA GCATATCTTT TCATACGTGT	1550
CTAGTTAATT TAAAGAATTA ATTATGACAT TTAGAATGAC TTCACITTTT	1600
TTACTTCTGC TCTGAGCAT AGATTGTATA GTAAAGTCAG AAAAACAAG	1650
CGCACAAACC CCAAGATGCT TAGCTGCTAA CAATAGCTTT CCACGGTCTG	1700
TGATGGTTAC TTTGAGCATC CGTAACTGGA ATACTAGTTC TAAAAAGGCT	1750
TCAGACTACT ACAATAGATC TACGTCTCCT TCGACTCTCC ATGCAATGA	1800
AGATCAAGAT AGATATCCTT CTGTGATTTG GGAAGCAAAG TGTGCTACT	1850
TAGGATGTGT TAATGCTGAT GCGAATGTAG ACTACCATAT GAACTCAGTC	1900
CCTATCCAAC AAGAGATTCT AGTGGTCCGC AAAGGCGATC AACCTGCTC	1950
TAATTCATTT AGGCTAGAGA AGATGCTAGT GACTGTAGGC TGCACATGCG	2000
TTACTCCCAT TGTTCCACAAT GTAGACTAAA AGCTATCTAA ATTTTGAAAA	2050
TTAACATTTC ACTAAAAAAC AAAAATTGA TTTTCTCTT TTAAATAAAA	2100
AAAGTTTAAT ATAAGTTCTG GCTTGTGTTG TTTTGGACTA ATCAATGTAG	2150
ATCACACTTG TGATCTTAGC TCTCGGGAAG CAATGTAAGA AAATATATTT	2200
AACTTAAGAG TTTTAGACTT GCTTGAGTTT TATGAGTAAA AAACAAAGAA	2250
TAAGCACAGC TTCTTGATC TTCTTTTAAA AACTTTAAGT TATTTATGTA	2300
TTTAATATAA TCTAATGTTT CTAAACATG TTGATTTGA GGTCCACTAA	2350
TACAACATTA TAATTTTTTC TGTATAACA CTTTTCGAAG AAGAACTCAT	2400
TTTATAGAAA ATGAGCAGTA TTCAAAAAAA ATGTTTGATA TGCTGTAATA	2450
TTGGAGAGGA AGAACTTTTA CAAGCATGTG ATTGTCCTAG CAGAGTCCAT	2500
CATACATGCT TACAAAGTCA	2520

Table 2, continued:

Predicted amino acid sequence (SEQ ID NO:4) of encoded protein of the  
related herpesvirus Saimiri open reading frame ORF13

~~Tml7. Peptide sequence~~

MTERM TSLVL LLLLS IDCIV KSEIT SAQTP RCLAA NNSFP RSVMV TLSIR 50

NWNTS SKRAS DYYNR STSPW TLHRN EDQDR YPSVI WEAKC RYLGC VNADG 100

NVDYH MNSVP IQQEI LVVRK GHQPC PNSFR LEKML VTVGC TCVTP IVHNV 150

D 151

MVIDG CKKYM RRTCG DVLBN LRGDC YQVLI EDCIP VLKMY AKEGR EFDYV 50

INDLT AVPIG TSPEE DSTWD FLRLI LDLSM KVLKQ DSKTF TQCNC VNLTE 100

ALSLY EEQLG RLYCP VEFCK EICV ISYLE LWVPY TVWKK AKP 143

Table 3: Nucleotide sequence (SEQ ID NO:5) of human CTLA-8 fragment and predicted amino acid sequence (SEQ ID NO:6) of encoded protein.

AGC/CGC AAT GAG GAC CCT GAG AGA TAT CCC TCT GTG ATC TGG GAG  
GCA AAG TGC CGC CAC TTG GGC TGC ATC AAC GCT GAT GGG AAC GTG  
GAC TAC CAC ATG AAC TCT GTC CCC ATC CAG CAA GAG ATC CTG GTC  
CTG CGC AGG GAG CCT CCA CAC TGC CCC AAC TCC TTC CGG CTG GAG  
AAG ATA CTG GTG TCC GTG GGC TGC ACC TGT GTC ACC CCG ATT GTC  
CAC CAT GTG GCC TAA

ser/arg asn glu asp pro glu arg tyr pro ser val ile trp glu  
ala lys cys arg his leu gly cys ile asn ala asp gly asn val  
asp tyr his met asn ser val pro ile gln gln glu ile leu val  
leu arg arg glu pro pro his cys pro asn ser phe arg leu glu  
lys ile leu val ser val gly cys thr cys val thr pro ile val  
his his val ala OCH

This ~~was~~ was used to isolate a full length clone from human (SEQ ID NO:7),  
shown below with its predicted amino acid sequence (SEQ ID NO:8); SEQ ID  
NO:5 ~~is~~ corresponds to nucleotides 272-510 of SEQ ID NO:3:

GG CACAAACTCA TCCATCCCA GTTGATTGGA A3AAATAACG	42
ATG ACT CTT GGG AAG ACC TCA TTG GTG TCA CTG CTA CTG CTG CTG	87
Met thr pro gly lys thr ser leu val ser leu leu leu leu leu	15
AGC CTG GAG GCC ATA GTG AAG GCA GCA ATC ACA ATC CCA CGA AAT	132
ser leu glu ala ile val lys ala gly ile thr ile pro arg asn	30
CCA GGA TGC CCA AAT TCT GAG GAC AAG AAC TTC CCC CGG ACT GTG	177
pro gly cys pro asn ser glu asp lys asn phe pro arg thr val	45
ATG GTC AAC CTG AAC ATC CAT AAC CGG AAT ACC AAT ACC AAT CCC	222
met val asn leu asn ile his asn arg asn thr asn thr asn pro	60
aaa AGG TCC TCA GAT TAC TAC AAC CGA TCC ACC TCA CCT TGG AAT	267
lys arg ser ser asp tyr tyr asn arg ser thr ser pro trp asn	75
CTC CAC CGC AAT GAG GAC CCT GAG AGA TAT CCC TCT GTG ATC TGG	312
leu his arg asn glu asp pro glu arg tyr pro ser val ile trp	90
GAG GCA AAG TGC CGC CAC TTG GGC TGC ATC AAC GCT GAT GGG AAC	357
glu ala lys cys arg his leu gly cys ile asn ala asp gly asn	105
GTG GAC TAC CAC ATG AAC TCT GTC CCC ATC CAG CAA GAG ATC CTG	402
val asp tyr his met asn ser val pro ile gln gln glu ile leu	120
GTC CTG CGC AGG GAG CCT CCA CAC TGC CCC AAC TCC TTC CGG CTG	447
val leu arg arg glu pro pro his cys pro asn ser phe arg leu	135
GAG AAG ATA CTG GTG TCC GTG GGC TGC ACC TGT GTC ACC CCG ATT	492
glu lys ile leu val ser val gly cys thr cys val thr pro ile	150
GTC CAC CAT GTG GCC TAA	510
val his his val ala OCH	155 156

Table 4: Nucleotide sequence (SEQ ID NO:9) of mouse CTLA-8 fragment and predicted amino acid sequence (SEQ ID NO:10) of encoded protein.

gagggtcaagtgcacccagcaccagctgatcaggacgcgaaacatgagtcaggaggagaggtttcatctg 69  
tgtctctgatgctgttgctgctgctgagcctggggctacagtggaaggcagcagcgatccctcaaa 138  
gtcagcgtgtgcacaaactgaggccaaggacttcctccagaatgtgaagggtcaacctcaaaagtcttta 207  
actccctTGGCGCAAAAGTGAGCTCCAGAAGgCCTCAGACTACCTCAACCGTTCCACGTCACCTGGA 276  
CTCTCCACCGCAATGAAGAcCCTGATAGATATCCTCTGTGATCTGGGAAACCTCAGTGCCTCCACCCAGC 345  
GCTGTGTCAATGCGGAGggaaagctggacacacatgaattctgttctcatccagcaagagatcctgg 414  
tctgaagagggagcctgagagctgccccttcactttcaggggtcgagaagatgctgggtgggTGTGGGCT 483  
GCACCTGGGTGGCTCGATTGTCCGCCAGGCAGCCTAAACAGAGACCCGCGCTGACCCCTAAGAAACC 552  
CCACGTTTCTCAGCAAACTTACTTGCATTTTTAAACAGTTCCTGTCTATTGATTTTCAAGCAAGAAATG 621  
TGGATTGAGAGCGAGATTGAGAAATTGTCTGCCCTCCACAATGAAAAGAAGGTGTAAAGGGGTCCCAAAC 690  
TGCTTCgsgtttggtttctgtggactttaaattatttgggtatttataatataccaagataactttga 759  
aggcgtaacttatttaatagaagtatctacattattattatgtttctttctgaagaagacaaaattcaag 828  
actcagaaattttattattttaaaaggtaagcctatatatttatatgagctatttatgaattctatttttt 897  
tcttcagttatttgaagtattagaacatgattttcAGATTACCTAGGGAAATCCTAAGTAAGATTAAA 966  
TATTAATGGAAATTTGAGCTTTACTATTGGTTGATTTAAGGTTCTCTCTCTGAATGGGGTGAAAACC 1035  
AAACTTAGTTTTATGTTTAATAACTTTTTAAATTATTGAAATTCAAAAAATTGATAATTTAGCTCC 1104  
TACTCTGTTTTAAAAAAAAAAAAAAAAAAAA 1134

Mouse CTLA-8 predicted amino acid sequence (SEQ ID NO:10). The mature polypeptide probably starts at a position about amino acid 19 (Leu) to amino acid 21 (Ala).

METSerProGlyArgAlaSerSerValSerLeuMETLeuLeuLeuLeuLeuSerLeuAlaAlaThrValLys 24  
AlaAlaAlaIleIleProGlnSerSerAlaCysProAsnThrGluAlaLysAspPheLeuGlnAsnValLys 48  
ValAsnLeuLysValPheAsnSerLeuGlyAlaLysValSerSerArgArgProSerAspTyrLeuAsnArg 72  
SerThrSerProTrpThrLeuHisArgAsnGluAspProAspArgTyrProSerValIleTrpGluAlaGln 96  
CysArgHisGlnArgCysValAsnAlaGluGlyLysLeuAspHisHisMETAsnSerValLeuIleGlnGln 120  
GluIleLeuValLeuLysArgGluProGluSerCysProPheThrPheArgValGluLysMETLeuValGly 144  
ValGlyCysThrCysValAlaSerIleValArgGlnAlaAla 158